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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

[illegible]

ATGACCGCTATGAGCACTGCAATTACACGCCAGATCGTTCTCGATACCGAAACCACCGGTATGAACCAGATTGGT 75

M T A M S T A I T R Q I V L D T E T T G M N O I G

GGCGCACTATGAAGGCCACAAGATCATTTGAGATTGGTGCCGTTGAAGTGGTGAACCGTCGCCTGACGGGCAATAAC 150

A H Y E G H K I I E I G A V E V V N R R L T G N N

TTCCATGTTTATCTCAAAACCCGATCGGCTGGTGGATCCGGAAGCCTTTGCGGTACATGGTATTGCCGATGAATTT 225

F H V Y L K P D R L V D P E A F G V H G I A D E E F

TTGCTCGATAAGCCACGTTTGCCGAAGTAGCCGATGAGTTCATGGACTATATTCGGGCGGAGTTGGTGATC 300

L L D K P T F A E V A D E F M D Y I R G A E L V I
 mutD

CATAACGCAGCGTTCGATATCGGCTTTATGGACTACGAGTTTTCGTTGCTTAAGCGGATATTCGAAGACCAAT 375

H N A A F D I G F M D Y E F S L L K R D I P K T N

FIG. 1A

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ACTTICTGTAAAGGTCACCGATAGCCTTGCGGTGGCGAGGAAATGTTTCCGGTAAGCGCAACAGCCTCGATGCG 450

_____mutD_____

T F C K V T D S L A V A R K M F P G K R N S L D A

TIATGTGCTCGCTACGAAATAGATAACAGTAAACGAACGCTGCACGGGCATTACTCGATGCCAGATCCTTGCG 525

_____mutD_____

L C A R Y E I D N S K R T L H G A L L D A Q I L A

GAAGTTIATCTGGCGATGACCGGTGGTCAACGTCGATGGCTTTTTCGATGGAAGGAGAGACACACAGCAACAA 600

_____mutD_____

E V Y L A M T G G O T S M A F A M E G E T Q Q Q Q

GGTGAAGCAACAATTTCAGCGCATTGTACGTCAGGCAAGTAAGTTACGCGTTGTTTTTTCGACAGATGAAGAGATT 675

_____mutD_____

G E A T I Q R I V R Q A S K L R V V F A T D E E I

GCAGCTCATGAAGCCCGTCTCGATCTGGTGCAGAGAAGCGGGAAGTTGCCTCTGGCGAGCATAA 741

_____mutD_____

A A H E A R L D L V O K K G G S C L W R A .

FIG..1B

FIG. 2A

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| | | |
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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

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|-----|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| 310 | 310 | 320 | 330 | 340 | 350 | 360 | |
| | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | |
| 310 | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | Eb_429T.dna |
| | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | GGCGGCA | Eb_GEBT.dna |
| 370 | 370 | 380 | 390 | 400 | 410 | 420 | |
| | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | |
| 370 | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | Eb_429T.dna |
| | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | CTGTACAGCTA | Eb_GEBT.dna |
| 430 | 430 | 440 | 450 | 460 | 470 | 480 | |
| | AACACCA | AACACCA | AACACCA | AACACCA | AACACCA | AACACCA | |
| 430 | AACACCA | AACACCA | AACACCA | AACACCA | AACACCA | AACACCA | Eb_429T.dna |
| | AACACCA | AACACCA | AACACCA | AACACCA | AACACCA | AACACCA | Eb_GEBT.dna |
| 490 | 490 | 500 | 510 | 520 | 530 | 540 | |
| | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | |
| 490 | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | Eb_429T.dna |
| | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | ACCAAAGTAA | Eb_GEBT.dna |
| 550 | 550 | 560 | 570 | 580 | 590 | 600 | |
| | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | |
| 550 | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | Eb_429T.dna |
| | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | CCGCTGCTGAT | Eb_GEBT.dna |

FIG._2B

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| | | |
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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

| | | | | | | |
|-----|---|-----|-----|-----|-----|-------------|
| 610 | 620 | 630 | 640 | 650 | 660 | |
| 610 | A C C C A C G C G G T A G A G C C C T A T A T C T C C A A A G A C G C C A A C C C G G T T A C C G A T G C C T C T G C T | | | | | Eb_429T.dna |
| 610 | A C C C A C G C G G T A G A G C C C T A T A T C T C C A A A G A C G C C A A C C C G G T T A C C G A T G C C T C T G C T | | | | | Eb_GEBT.dna |
| 670 | 680 | 690 | 700 | 710 | 720 | |
| 670 | A T T C A G G C C A T C A A A C T G A T T G C C A C C A A C T T G C G C C A G G C C G T C G C C C T G G G A C C A A C | | | | | Eb_429T.dna |
| 670 | A T T C A G G C C A T C A A A C T G A T T G C C A C C A A C T T G C G C C A G G C C G T C G C C C T G G G A C C A A C | | | | | Eb_GEBT.dna |
| 730 | 740 | 750 | 760 | 770 | 780 | |
| 730 | C T C A A A G C C C G T G A A A C A T G G C C C T G C G C C T C T C T G C T G G C C G G G A T G G C C T T T A A C A A C | | | | | Eb_429T.dna |
| 730 | C T C A A A G C C C G T G A A A C A T G G C C C T G C G C C T C T C T G C T G G C C G G G A T G G C C T T T A A C A A C | | | | | Eb_GEBT.dna |
| 790 | 800 | 810 | 820 | 830 | 840 | |
| 790 | G C C A A C C T G G G C T A T G T T C A C G C C C A T G G C C T C A C C A G C T G G G C G G C C C T G T A C G A C A T G G C C | | | | | Eb_429T.dna |
| 790 | G C C A A C C T G G G C T A T G T T C A C G C C C A T G G C C T C A C C A G C T G G G C G G C C C T G T A C G A C A T G G C C | | | | | Eb_GEBT.dna |
| 850 | 860 | 870 | 880 | 890 | 900 | |
| 850 | C A C G G G G T G G C G A A C G C G G G T C C T G C T G C C C C C A T G T C T G C C G C T A T A A C C T G A T T G C C C A A C | | | | | Eb_429T.dna |
| 850 | C A C G G G G T G G C G A A C G C G G G T C C T G C T G C C C C C A T G T C T G C C G C T A T A A C C T G A T T G C C C A A C | | | | | Eb_GEBT.dna |

FIG..2C

| | | |
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| APPROVED BY DRAFTSMAN | O.G. FIG. | |
| | CLASS | SUBCLASS |

[illegible]

| | | | | | | | |
|------|-------|---------|-----------|-------------------|----------|---------|----------|
| 910 | 910 | 920 | 930 | 940 _{yr} | 950 | 960 | |
| | CCGGA | AAATTTG | CCGATATCG | CCACCTTTAT | GGGGA | AAACAC | CCCGGTC |
| 910 | CCGGA | AAATTTG | CCGATATCG | CCACCTTTAT | GGGGA | AAACAC | CCCGGTC |
| | CCGGA | AAATTTG | CCGATATCG | CCACCTTTAT | GGGGA | AAACAC | CCCGGTC |
| 970 | 970 | 980 | 990 | 1000 | 1010 | 1020 | |
| | ATGGA | CGCAG | CGGAGCT | GGCCATCAG | CGCCATTG | CCCCGTC | TGTC |
| 970 | ATGGA | CGCAG | CGGAGCT | GGCCATCAG | CGCCATTG | CCCCGTC | TGTC |
| | ATGGA | CGCAG | CGGAGCT | GGCCATCAG | CGCCATTG | CCCCGTC | TGTC |
| 1030 | 1030 | 1040 | 1050 | 1060 | 1070 | 1080 | |
| | CCGCA | GCACCTG | CGTGAACT | GGGGGTAA | AGAGCG | CCGACTT | CCCGTACA |
| 1030 | CCGCA | GCACCTG | CGTGAACT | GGGGGTAA | AGAGCG | CCGACTT | CCCGTACA |
| | CCGCA | GCACCTG | CGTGAACT | GGGGGTAA | AGAGCG | CCGACTT | CCCGTACA |
| 1090 | 1090 | 1100 | 1110 | 1120 | 1130 | 1140 | |
| | GCCCT | GAAAGAC | GGCAACG | CCCTTCTCTA | ACCCGCG | CAAGGG | AACGAA |
| 1090 | GCCCT | GAAAGAC | GGCAACG | CCCTTCTCTA | ACCCGCG | CAAGGG | AACGAA |
| | GCCCT | GAAAGAC | GGCAACG | CCCTTCTCTA | ACCCGCG | CAAGGG | AACGAA |
| 1150 | 1150 | 1160 | 1170 | | | | |
| | GACAT | TTTCC | GGCCAGG | CAATTC | CTGA | | |
| 1150 | GACAT | TTTCC | GGCCAGG | CAATTC | CTGA | | |
| | GACAT | TTTCC | GGCCAGG | CAATTC | CTGA | | |

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG. 2D

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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

MSYRMFDYLVNPNFPGPGAVSVVGQRCQLLGGKKALLVT
MSYRMFDYLVNPNFPGPGAVSVVGQRCQLLGGKKALLVT

| | | | | | |
|-----|--|-----|-----|-----|-------------|
| 10 | 10 | 40 | 70 | 100 | |
| 10 | MSYRMFDYLVNPNFPGPGAVSVVGQRCQLLGGKKALLVT | | | | Eb_429T.dna |
| 10 | MSYRMFDYLVNPNFPGPGAVSVVGQRCQLLGGKKALLVT | | | | Eb_GEBT.dna |
| | 130 | 160 | 190 | 220 | |
| 130 | DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGV EPNPKDTN | | | | Eb_429T.dna |
| 130 | DKGLRAIKDGAVDQTVKHLKAAGIEVVIFDGV EPNPKDTN | | | | Eb_GEBT.dna |
| | 250 | 280 | 310 | 340 | |
| 250 | VLDGLAMFRKEQC DMIITVGGGSPHDCGKGIGIAATHPGD | | | | Eb_429T.dna |
| 250 | VLDGLAMFRKEQC DMIITVGGGSPHDCGKGIGIAATHPGD | | | | Eb_GEBT.dna |
| | 370 | 400 | 430 | 460 | |
| 370 | LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK | | | | Eb_429T.dna |
| 370 | LYSYAGIETLTNPLPPIIAVNTTAGTASEVTRHCVLTNTK | | | | Eb_GEBT.dna |
| | 490 | 520 | 550 | 580 | |
| 490 | TKVKKFVIVSWRNLPSPVSINDP LLMIGKPA GLTAATGMDAL | | | | Eb_429T.dna |
| 490 | TKVKKFVIVSWRNLPSPVSINDP LLMIGKPA GLTAATGMDAL | | | | Eb_GEBT.dna |

FIG._3A

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| | | |
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| APPROVED | O.G. FIG. | |
| BY | CLASS | SUBCLASS |
| DRAFTSMAN | | |

| | | | | | |
|------|---------------------|------|------|------|-------------|
| 610 | THAVEAYISKDANPVT | 640 | 670 | 700 | |
| 610 | THAVEAYISKDANPVT | 640 | 670 | 700 | Eb_429T.dna |
| | THAVEAYISKDANPVT | 640 | 670 | 700 | Eb_GEBT.dna |
| 730 | LKARENMACASLLAGMAFN | 760 | 790 | 820 | |
| 730 | LKARENMACASLLAGMAFN | 760 | 790 | 820 | Eb_429T.dna |
| | LKARENMACASLLAGMAFN | 760 | 790 | 820 | Eb_GEBT.dna |
| 850 | HGVANAVLLPHVCRYNLI | 880 | 910 | 940 | |
| 850 | HGVANAVLLPHVCRYNLI | 880 | 910 | 940 | Eb_429T.dna |
| | HGVANAVLLPHVCRYNLI | 880 | 910 | 940 | Eb_GEBT.dna |
| 970 | MDAAELAISAIARLSKDV | 1000 | 1030 | 1060 | |
| 970 | MDAAELAISAIARLSKDV | 1000 | 1030 | 1060 | Eb_429T.dna |
| | MDAAELAISAIARLSKDV | 1000 | 1030 | 1060 | Eb_GEBT.dna |
| 1090 | ALKDGNAPSNPRKGNKEI | 1120 | 1150 | | |
| 1090 | ALKDGNAPSNPRKGNKEI | 1120 | 1150 | | Eb_429T.dna |
| | ALKDGNAPSNPRKGNKEI | 1120 | 1150 | | Eb_GEBT.dna |

Decoration 'Decoration #1': Shade (with solid black) residues that differ from the Consensus.

FIG._3B

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| | | |
|-----------|-----------|----------|
| APPROVED | O.G. FIG. | |
| | CLASS | SUBCLASS |
| BY | | |
| DRAFTSMAN | | |

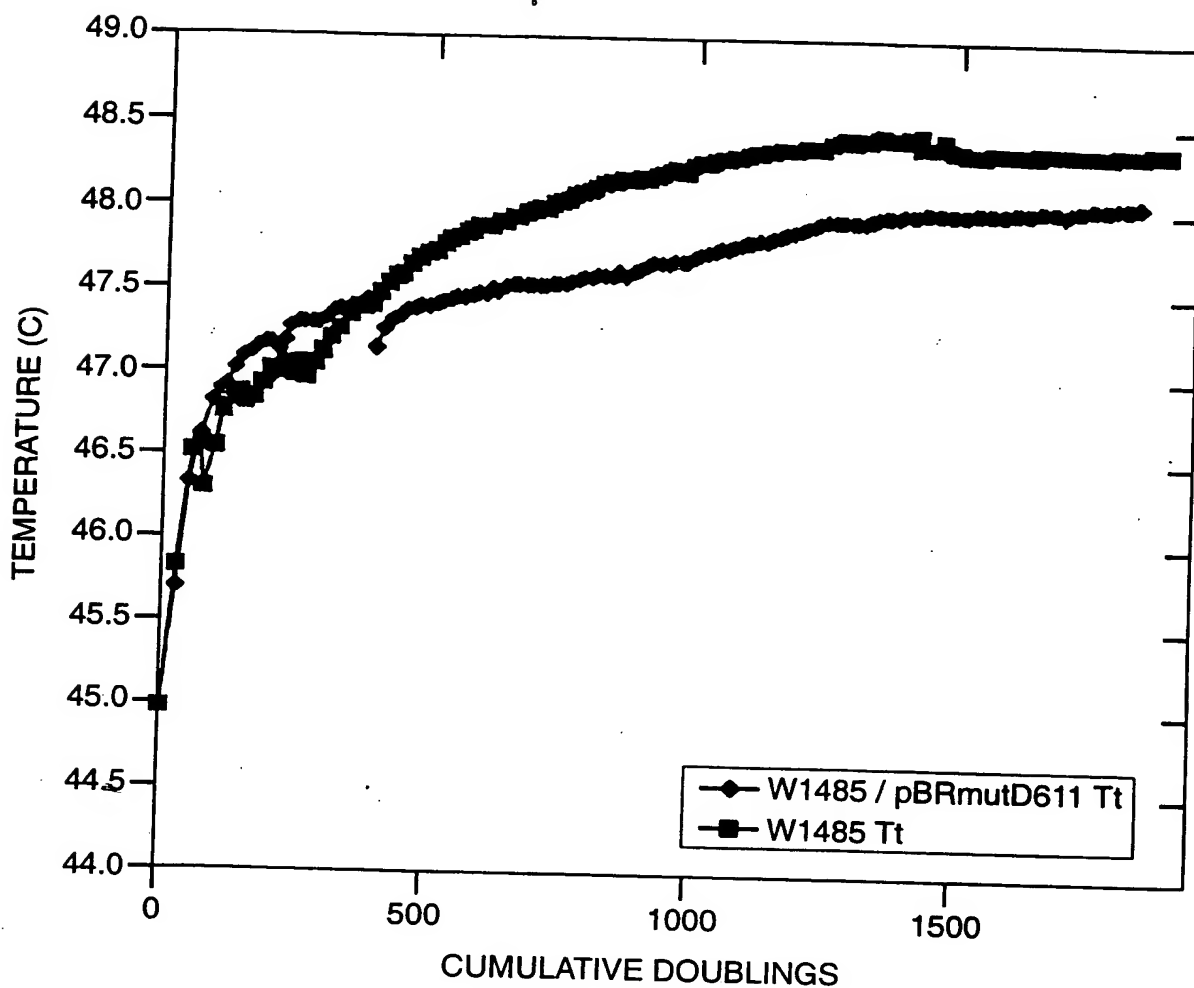


FIG._4

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| | | |
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| APPROVED | O.G. FIG. | |
| | CLASS | SUBCLASS |
| BY | | |
| DRAFTSMAN | | |

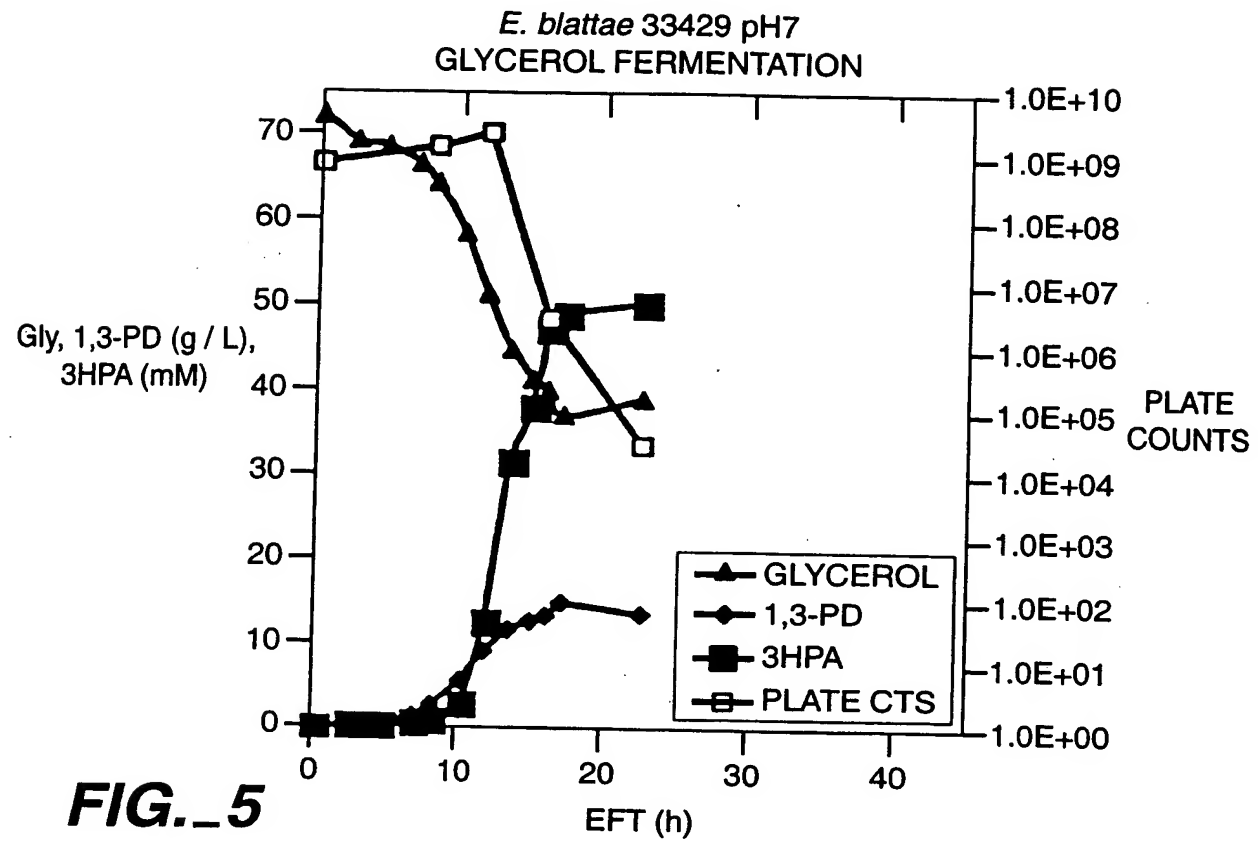


FIG._5

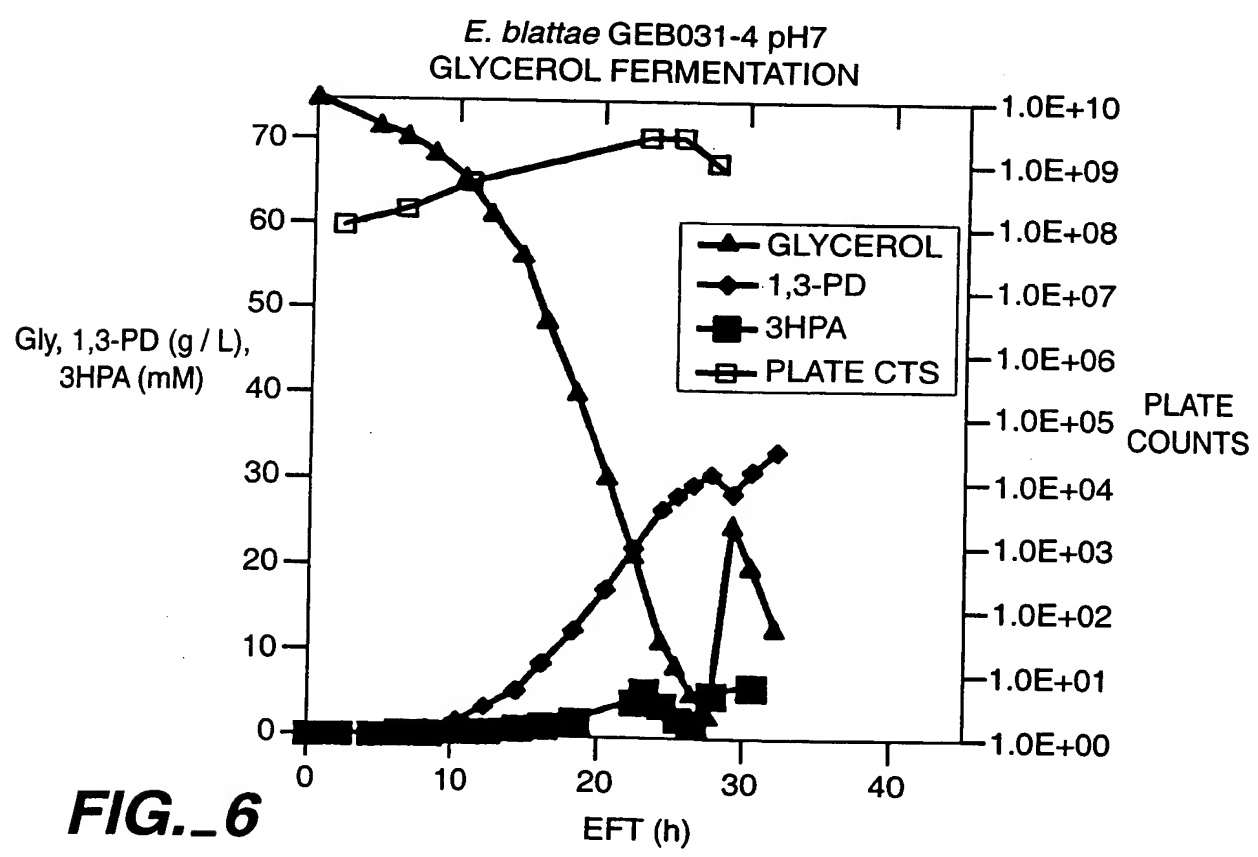


FIG._6